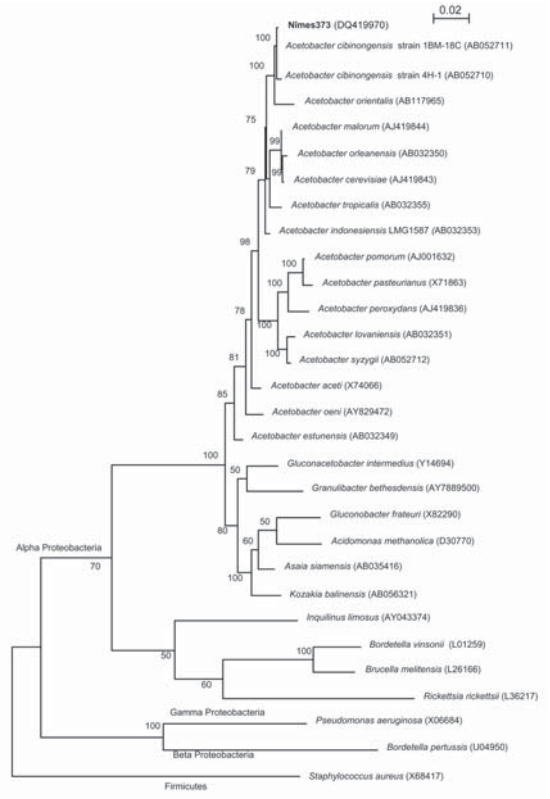

Figure. 16S rDNA maximum-likelihood phylogenetic tree showing the relationships of the isolate nîmes373 with 15 species of the genus *Acetobacter* and 6 strains representative of the 6 other genera of acetic acid bacteria in the Alpha Proteobacteria. Sequences of Alpha, Beta, and Gamma Proteobacteria of clinical relevance were also included in the tree. *Staphylococcus aureus* (*Firmicutes*) 16S rDNA was used as an outgroup. The 16S rDNA sequences used to reconstruct this tree were obtained from the GenBank database, and their accession numbers are indicated in brackets. The tree was reconstructed using DNAML from the PHYLIP package v. 3.6.6, on the basis of the F84 (+ gamma distribution + invariant sites) substitution model. The scale bar indicates 0.02 substitutions per nucleotide position. Numbers given at the nodes represent bootstrap percentages calculated on 100 replicates.

genicity (*10*). This second known report of human infection with acetic acid bacteria should alert clinicians to the risk for opportunistic infections with these bacteria, which are broadly used in food processing.

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Risk for Epidemics after Natural Disasters

To the Editor: Myths that disaster-affected populations are at high risk for outbreaks and that dead bodies contribute to this risk are common (*1*). Conversely, some experts deny high, short-term risk after disasters (*2*).

We agree with Watson et al. (*3*) that the risk for communicable diseases

transmission after natural disasters is low but real and that it is not directly related to the disasters and dead bodies, but primarily associated with the characteristics of the displaced population within the local disease ecology. This belief supports the need for rapid but accurate assessment of health status, risk, and needs, the results of which greatly influence the nature of relief activities (*4*). Key functions of relief teams are communicable diseases surveillance, early warning, and rapid response to epidemic-prone situations or outbreaks.

As an example, on October 26, 2005, after an earthquake in Pakistan, the World Health Organization asked the French military epidemiologic assessment team (1 epidemiologist and 1 veterinarian) to perform a sanitary assessment after cases of acute bloody diarrhea were reported in the camp of Tariqabad (estimated population ≈2,000), near Muzaffarabad. The assessment highlighted a lack of safe water and sanitation facilities, low routine immunization coverage, and disruption of healthcare services.

To prevent further diarrhea, we recommended improving the overall water and sanitation conditions. A medical team from a French nongovernment organization was also provided to help the 1 physician at the camp. Concurrently, we recommended a vaccination campaign as preventive strategy against diseases likely to occur in such conditions: tetanus, diphtheria, and measles. These measures were quickly implemented to reduce the overall risk, and no further unusual increases in disease incidence were noted during the following weeks. As in another outbreak documented in a camp in the Muzaffarabad area (*5*), rapid detection, response, and implementation of control measures are critical for minimizing the illness and death associated with outbreaks in these high-risk populations.

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Recombinant Sapovirus Gastroenteritis, Japan

To the Editor: Sapovirus and norovirus are causative agents of gastroenteritis in children and adults. Norovirus is the most important cause of outbreaks of gastroenteritis, whereas only a few outbreaks of sapovirus have been reported (*1*,*2*). On the basis of complete capsid gene sequences, sapovirus can be divided into 5 genogroups, among which GI, GII, GIV, and GV infect humans, whereas sapovirus GIII infects porcine species.

We report 2 outbreaks of gastroenteritis in Hokkaido, Japan. The first outbreak (A) occurred at a college from May 29 to June 2, 2000. A total of 12 persons (11 students and 1 teacher) reported symptoms of gastroenteritis (nausea, vomiting, stomachache, diarrhea, and fever); 11 stool specimens were collected from days 1 to 7 after onset of illness (Table). These specimens were negative for norovirus (data not shown), but 5 were positive for sapoviruslike viruses by electron microscopy (Table).

The 11 specimens were then examined for sapovirus by using nested reverse transcription–PCR (RT-PCR) as described (*3*). A total of 9 (82%) of 11 specimens were positive for sapovirus. Sequence analysis showed that these 9 viruses had 100% nucleotide identity and likely represented the same sapovirus strain (termed Yak2 strain, GenBank accession no. AB046353). To determine the number of cDNA copies per gram of stool, we performed real-time RT-PCR as described (*4*). The number of sapovirus cDNA copies ranged from 5.36×10^5 to 7.47×10^9/g stool (median 5.49×10^9 copies/g stool) (Table).

The second outbreak (B) occurred at a kindergarten from February 1 to 22, 2005. A total of 23 persons (15 children and 8 adults) reported symp-